

SEQUENCE LISTING

(1) GENERAL INFORMATION

5 (i) APPLICANT: Lincoln, Steve
Klinger, Tod M.
Au-Young, Janice
Tang, Y. Tom
Goold, Richard
10 Akerblom, Ingrid E.
Seilhamer, Jeffrey J.
Hawkins, Phillip R.
Murry, Lynn E.
Delegeane, Angelo M.
15 Levine, Wendy B.
Hillman, Jennifer L.
Goli, Surya K.
Altus, Christina M.
Bandman, Olga
20 LaBrie, Samuel T.
Shah, Purvi

25 (ii) TITLE OF THE INVENTION: Database for Storage and Analysis of Full Length Sequences

(iii) NUMBER OF SEQUENCES: 10

30 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Bozicevic & Reed, L.L.P.
(B) STREET: 285 Hamilton Ave.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: U.S.
35 (F) ZIP: 94301

(v) COMPUTER READABLE FORM:

40 (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

45 (A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

50 (A) APPLICATION NUMBER: 08/282,955
(B) FILING DATE: July 29, 1995

(A) APPLICATION NUMBER: 08/187,530
(B) FILING DATE: January 27, 1994

55 (A) APPLICATION NUMBER: 08/179,873
(B) FILING DATE: January 11, 1994

(A) APPLICATION NUMBER: 08/100,523

(B) FILING DATE: August 3, 1993

(A) APPLICATION NUMBER: 07/977,780
(B) FILING DATE: November 19, 1992

5 (A) APPLICATION NUMBER: 07/916,491
(B) FILING DATE: July 17, 1992

10 (A) APPLICATION NUMBER: 08/289,822
(B) FILING DATE: August 12, 1994

(A) APPLICATION NUMBER: 08/581,240
(B) FILING DATE: December 29, 1995

15 (A) APPLICATION NUMBER: 08/657,697
(B) FILING DATE: May 29, 1996

(A) APPLICATION NUMBER: 08/747,547
(B) FILING DATE: November 12, 1996

20 (A) APPLICATION NUMBER: 08/712,710
(B) FILING DATE: September 12, 1996

25 (A) APPLICATION NUMBER: 08/744,026
(B) FILING DATE: November 5, 1996

(A) APPLICATION NUMBER: 08/786,999
(B) FILING DATE: January 23, 1997

30 (A) APPLICATION NUMBER: 08/822,262
(B) FILING DATE: March 20, 1997

(A) APPLICATION NUMBER: 08/000,000 (as yet unassigned)
(B) FILING DATE: October 16, 1997

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Francis, Carol L.
(B) REGISTRATION NUMBER: 36,513
(C) REFERENCE/DOCKET NUMBER: 6514/069001

40 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-327-3400
(B) TELEFAX: 650-327-3231

45 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: Pancreatic Cancer

(B) CLONE: PANC1A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	GTACGGAGGT GAGGTTGTN ACCCGGATTC TAAGAGGTGG GCTTTAGTC CCTCCAGACC	60
	TCGGCTTAG TGCTGTCTCC GCTTTTCTT CACCTTCACA GAGGTTCGTG TCTTCCTAAA	120
	AGAAGGTTTT ATTGGGAGGT AAAGGTCAAT GCGTAGGGGT AGAGTAAGAT GTCTTATGGT	180
	GAAATTRAAG GTAAATTCTT GGGACCTAGA GAAGAAGTAA CGAGTGAGCC ACGCTGTAAA	240
10	AAATTGAAGT CAACCCACAGA GTCGTATGTT TTCACAAATC ATAGTAATGC TGATTTCAC	300
	AGNATCCAAG AGAAAATGG AAATGATTGG GTCCCTGTGN NCATCATTGA TGTCAGAGGA	360
	CATAGTTATT TGC	373

(2) INFORMATION FOR SEQ ID NO:2:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Pancreatic Cancer
- (B) CLONE: PANC1B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30

GTGAGGTTG TTACCNCGAT TCTGAGAGGT GGGCTTTAG TCCCTCCAGA CCTCGGCTTT	60
AGTGCTGTCT CCGMTTTCTT TTCACCTTCA CAGAGATGTC TTATGGTGAA ATTGAAGGTA	120
AATTCTTGGG ACCTAGWGAA GAAGTAACGA GTGAGGCCACG CTGTAAAAAA TTGAAGTCAA	180
CCACAGAGCT GTATGTTTT CACAATCATA GTAATGCTGA TTTTCACAGW ATCCAAGAGA	240
AAACTGGAAA TGATTGGGT CCCTGTGACC ATCATTNATG TCAGAGGNCA TAGTTAATT	300
35 GCAGGAGANC AAAAATCAAA A	321

35

(2) INFORMATION FOR SEQ ID NO:3:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

50

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: NEUTGMT01
- (B) CLONE: 637393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

55

ATGACAGACT GTGAATTGAG ATATATTAC AGGCTGGCTC AGGACTATCT GCAGTGCCTC	60
CTACAGATAAC CACAAACCTGG ATCAGGTCCA AGCAAAACGT CCAGAGTGCT ACAAAATGTT	120
GGCGTTCTCAG TCCAAAAAGA AGTGGAAAAG AATCTGAAGT CATGCTTGGAA CAATGTTAAT	180
GTTGTGTCCG TAGACACTGC CAGAACACTA TTCAACCAAG TGATGGAAAA GGAGTTTGAA	240
GACGACATCA TTAACGGGG AAGAATTGTA ACCATATTG CATTGAGG TATTCTCATC	300

AAGAAACTTC	TACGACAGCA	AATTGCCCG	GATGTGGATA	CCTATAAGGA	GATTCATAT	360
TTTGTGCGG	AGTCATAAT	GAATAACACA	GGAGAATGGA	TAAGGCAAAA	CGGAGGCTGG	420
GAAAATGGCT	TTGTAAAGAA	GTGAAACCT	AAATCTGGCT	GGATGACTTT	TCTAGAAGTT	480
ACAGGAAAGA	TCTGTGAAAT	GCTATCTCTC	CTGAAGCAAT	ACTGTTGA		528

5

(2) INFORMATION FOR SEQ ID NO:4:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20	GTCCAAATCA	CTCATTGTTT	GTGAAAGCTG	AGTCACAGC	AAAACAAGCC	ACCATGAAGC	60
	TGTCGGTGTG	TCTCTGCTG	GTCACGCTGG	CCCTCTGCTG	CTACCAGGCC	AATGCCGAGT	120
	TCTGCCAGC	TCTTGTTCCT	GAGCTGTTAG	ACTTCTTCTT	CATTAGTGA	CCTCTGTTCA	180
	AGTTAAGTCT	TGCCAAATTT	GATGCCCTC	CGGAAGCTGT	TGCAGCCAAG	TTAGGAGTGA	240
25	AGAGATGCAC	GGATCAGATG	TCCCTTCAGA	AACGAAGCCT	CATTGCGGAA	GTCCTGGTGA	300
	AAATATTGAA	GAAATGTAGT	GTGTGACATG	AAAAAACTTT	CATCCTGGTT	TCCACTGTCT	360
	TTCAATGACA	CCCTGATCTT	CACTGCAGAA	TGTAAAGGTT	TCAAC		405

30 (2) INFORMATION FOR SEQ ID NO:5:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	GATCCTTGCC	ACCCGCGACT	GAACACCGAC	AGCAGCAGCC	TCACCATGAA	GTTGCTGATG	60
	GTCCTCATGC	TGGCGCCCT	CTCCCAGCAC	TGCTACGCAG	GCTCTGGCTG	CCCCTTATTG	120
	GAGAATGTGA	TTTCCAAGAC	AATCAATCCA	CAAGTGTCTA	AGACTGAATA	CAAAGAACTT	180
45	CTTCAAGAGT	TCATAGACGA	CAATGCCACT	ACAAATGCCA	TAGATGAATT	GAAGGAATGT	240
	TTTCTTAACC	AAACGGATGA	AACTCTGAGC	AATGTTGAGG	TGTTTATGCA	ATTAATATAT	300
	GACAGCAGTC	TTTGTGATT	ATTTAACCT	TCTGCAAGAC	CTTGGCTCA	CAGAACTGCA	360
	GGGTATGGTG	AGAAACCAAC	TACGGATTGC	TGCAAACAC	ACCTTCTCTT	TCTTATGTCT	420
50	TTTACTACA	AACTACAAGA	CAATTGTTGA	AACCTGCTAT	ACATGTTAT	TTAATAAAAT	480
	TGATGGCAAA	AACTG					495

(2) INFORMATION FOR SEQ ID NO:6:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY:
 (B) CLONE: Consensus

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCCCGCCG	CGCCCGGCGC	GCCCCGCCGC	CGGGGGGATG	TCTTACAAAC	CGAACTTGGC	60
CGCGCACATG	CCCGCCGCCG	CCCTCAACGC	CGCTGGGAGT	GTCCACTCGC	CTTCCACCA	120
CATGGCAACG	TCTTCACAGT	ACCGCCAGCT	GCTCAGTGAC	TACGGGCCAC	CGTCCCTAGG	180
15 CTACACCCAG	GGAACTGGGA	ACAGCCAGGT	GCCCCAAAGC	AAATACGCGG	AGCTGCTGGC	240
CATCATTGAA	GAGCTGGGGA	AGGAGATCAG	ACCCACGTAC	GCAGGGAGCA	AGAGTGCAT	300
GGAGAGGCTG	AAGCGCGGCA	TCATTACACG	TAGAGGACTG	GTTCGGGAGT	TCTTGGCAGA	360
AACGGAACGG	AATGCCAGAT	CCTAGCTGCC	TTGTTGGTTT	TGAAGGATT	CCATCTTTT	420
ACAAGATGAG	AAGTTACAGT	TCATCTCCC	TGTTCAAGATG	AAACCCCTGT	TTTCAAAATG	480
20 GTTACAGTTT	CGTTTTCC	CCCATGGTTC	ACTTGGCTCT	GAACCTACAG	TCTCAAAGAT	540
TGAGAAAAGA	TTTGCAGTT	AATTAGGATT	TGCAATTAA	GTAGTTAGGA	ACTGCCAGG	600
TTTTTTTGT	TTTTTAAGCA	TTGATTAAA	AGATGCACGG	AAAGTTATCT	TACAGCAAAC	660
TGTAGTTGC	CTCCAAGACA	CCATTGTCTC	CCTTTAATCT	TCTCTTTGT	ATACATTGT	720
25 TACCCATGGT	GTTCTTGTT	CCTTTTCATA	AGCTAATACC	ACTGTAGGGA	TTTTGTTTG	780
AACGCATATT	GACAGCACGC	TTTACTTAGT	AGCCGGTTC	CATTGCCAT	ACAATGTAGG	840
TTCTGCTTAA	TGTAACATTCT	TTTTGCTTA	AGCATTGCA	TGACTATTAG	TGCTTCAAAG	900
TCAATTTTA	AAAATGCACA	AGTTATAAT	ACAGAAGAAA	GAGCAACCCA	CCAAACCTAA	960
CAAGGACCCC	CGAACACTTT	CATACTAAGA	CTGTAAGTAG	ATCTCAGTC	TGCGTTTATT	1020
30 GTAAAGTTGAT	AAAAACATCT	GGAAGAAAAT	GACTAAAAT	GTTCGCATCT	TTGTATGTAT	1080
TTATTACTTG	ATGTAATAAA	GCTTATTTC	ATTAACAATT	TGTATTAAA	TGTGGGTTCC	1140
	TTG					1143

35 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 871 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY:
 (B) CLONE: Consensus

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

50 ACCTGCTGGC	CCCTGGACAC	CTCTGTCACC	ATGTGGTTCC	TGGTTCTGTG	CCTCGCCCTG	60
TCCCTGGGGG	GGACTGGTGC	TGCGCCCCCG	ATTCACTCCC	GGATTGTGGG	AGGCTGGGAG	120
TGTGAGCAGC	ATTCCCAGCC	CTGGCAGCG	GCACCTGGTCA	TGGAAAACGA	ATTGTTCTGC	180
TCGGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTT	CCAGAACTCC	240
55 TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	300
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCCTGCT	CGCTAACGAC	360
CTCATGNTCA	TCAAGTTGGA	CGAATCCGT	TCCGAGTCTG	ACAACATCCG	GAGNATCAGC	420
ATTGNTTCGC	AGTGCCCTAC	CGCGGGGAAC	TTTGCCTCG	TTTCTGGCTG	GGGTCTGCTG	480

5	GCGAACGGCA	GAATGCCTAC	CGTGCTGCAG	TGCGTGAACG	TGTCGGTGGT	GTCTGAGGAG	540
	GTCTGCAGTA	AGCTCTATGA	CCCGCTGTAC	CACCCCAGCA	TGTTCTGCGC	CGGCAGGAGGG	600
	CAAGACCAGA	AGGACTCCTG	CAACGGTGAC	TCTGGGGGGC	CCCTGATCTG	CAACGGGTAC	660
	TTGCAGGGCC	TTGTGTCTTT	CGGAAAAGCC	CCGTGTGGCC	AAGTTGGCGT	GCCAGGTGTC	720
	TACACCAACC	TCTGCAAATT	CACTGAGTGG	ATAGAGAAAA	CCGTCCAGGC	CAGTTAACTC	780
	TGGGGACTGG	GAACCCATGA	AATTGACCCC	CAAATACATC	CTGCGGAAGG	AATTCAAGGAA	840
	TATCTGTTCC	CAGCCCCCTCC	TCCCTCAGGC	C			871

10 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Colnnot01
- 20 (B) CLONE: 609476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25	GGCCGGGTTG	GGGGTGTGCG	ATTGTGTGGG	ACGGTCTGGG	GCAGCCCAGC	ACGGGCTGAC	60
	CCTCTGCCCTG	CGGGGAAGGG	AGTCGCCAGG	CGGCCGTCA	GGCGGTGTCG	GAGAGCCAGC	120
	TCAAGAAAAT	GGTGTCCAAG	TACAAATACA	GAGACCTAAC	TGTACGTGAA	ACTGTCAATG	180
	TTATTACTCT	ATACAAAGAT	CTCAAACCTG	TTTGGATT	ATATGTTTT	AACGATGGCA	240
	GTTCCAGGGAA	ACTAATGAAC	CTCACTGGAA	CAATCCCCTG	GCCTTATAGA	GGTAATACAT	300
30	ACAATATTCC	AATATGCCTA	TGGCTACTGG	ACACATACCC	ATATAATCCC	CCTATCTGTT	360
	TTGTTAAGCC	TACTAGTTCA	ATGACTATTA	AAACAGGAAA	GCATGTGAT	GCAAATGGGA	420
	AGATATATCT	TCCTTATCTA	CATGAATGGA	AACACCCACA	GTCAGACTTG	TTGGGGCTTA	480
	TTCAGGTCTAT	GATTGTGGTA	TTTGGAGATG	AACCTCCAGT	CTTCTCTCGT	CCTATTTCGG	540
	CATCCTATCC	GCCATACCCAG	GCAACGGGGC	CACCAAATAC	TTCCCTACATG	CCAGGCATGC	600
35	CAGGTGGAAT	CTCTCCATAC	CCATCCGGAT	ACCCCTCCAA	TCCCAGTGTT	TACCCAGGCT	660
	GTCCTTACCC	ACCTGGTGGT	CCATATCCTG	CCACAACAAG	TTCTCAGTAC	CCCTCTCAGC	720
	CTCCTGTGAC	CACTGTTGGT	CCCAGTAGGG	ATGGCACAAT	CAGCGAGGAC	ACCATCCGAG	780
	CCTCTCTCAT	CTCTCGGGTC	AGTGACAAAC	TGAGATGGCG	GATGAAGGAG	GAAATGGATC	840
	GTGCCCGAGGC	AGAGCTCAAT	GCCTTGAAAC	GAACAGAAGA	AGACCTGAAA	AAGGGTCACC	900
40	AGAAAATGGA	AGAGATGGTT	ACCCGTTTAG	ATCAAGAAGT	AGCCGAGGTT	GATAAAAACA	960
	TAGAACTTTT	AAAAAAGAAG	GATGAAGAAC	TCAGTTCTGC	TCTGGAAAAA	ATGGAAAATC	1020
	AGTCTGAAAAA	CAATGATATC	GATGAAGTTA	TCATTCCAC	AGCTCCCTTA	TACAAACAGA	1080
	TCCTGAATCT	GTATGCAGAA	GAAAACGCTA	TTGAAGACAC	TATCTTTAC	TTGGGAGAAG	1140
	CCTTGAGAAG	GGCGGTGATA	GACCTGGATG	TCTTCTGAA	GCATGTACGT	CTTCTGTCCC	1200
45	GTAAACAGTT	CCAGCTGAGG	GCACTAATGC	AAAAAGCAAG	AAAGACTGCC	GGTCTCAGTG	1260
	ACCTCTACTG	ACTTCTCTGA	TACCAGCTGG	AGGGTGAGCT	CTTCTTAAAG	TATTCTTCTC	1320
	TTCCTTTAT	CAGTAGGTGC	CCAGAATAAG	TTATTGCAGT	TTATCATTCA	MGTGTAAAAT	1380
	ATTTTGAATC	AATAATATAT	TTTCTGTTT	CTTTGGTAA	AGATGGAT		1428

50 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- 55 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THPINOT03
 (B) CLONE: 2446131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5	GGCTGAGCGG	CCCCGAGCC	AACCCCCGAG	GAGCGGCCGG	CTGGCGTCCG	CCGCGCCCG	60
	GAGTTGGGGA	TGTCCTACAA	ACCCATCGCC	CCTGCTCCCA	GCAKCACCCC	TGGCTCCAGC	120
	ACCCCTGGGC	CGGGCACCCC	GGTCCCTACA	GGAAAGCGTCC	CGTCGCCGTC	GGGCTCAGTG	180
10	CCAGGAGCGG	GGCCTCCTT	CAGACCGCTG	TTAACGACT	TTGGACCGCC	TTCCATGGGC	240
	TACGTGCAGG	CGATGAAGCC	ACCCGGCGCC	CAGGGCTCCC	AGAGCACCTA	CACGGACCTG	300
	CTGTCAGTCA	TAGAGGAGAT	GGGCAAAGAG	ATCCGGCCTA	CCTATGCTGG	CAGCAAGAGC	360
	GCCATGGAGC	GCCTGAAGAG	AGGTATCATC	CATGCCCGGG	CCCTAGTCAG	AGAGTGCCTG	420
	GCAGAGACAG	AGCGGAACGC	CCGCACGTAA	CAGGAAGCGC	CTCGGCCTCA	GCGTCTGGAC	480
15	CTATCCGGCC	ACTGCAGAGC	ACCCGCTCT	CCCTGGCCTT	CATCCCAGT	TGCACTAACCC	540
	ATCCTGGGCT	TCCTGTCTG	TGTCCCTGG	TGGGTCCCCT	CCAGGAACCA	AGGAGTGGCC	600
	CTCCAGGTGG	CAGCACTAAG	GACACCCCCC	CACACAAGA	GTTAGCAGCG	AGGTCCCCAT	660
	GAGTCCC						667

(2) INFORMATION FOR SEQ ID NO:10: -

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30	CTGAACTCTA	CCTGGTGACC	AGGGACCAGG	ACCTTTATAA	GGTGGAAAGGC	TTGATGTCCT	60
	CCCCAGACTC	AGCTCCTGGT	GAAGCTCCA	GCCATCAGCC	ATGAGGGTCT	TGTATCTCCT	120
	CTTCTCGTTC	CTCTTCATAT	TCCTGATGCC	TCTTCCAGGT	GTTTTTGGTG	GTATAGGCAGA	180
	TCCCGTTACC	TGCCTTAAGA	GTGGAGCCAT	ATGTCATCCA	GTCTTTGCC	CTAGAAGGTA	240
35	TAAACNAATT	GGCACCTGTG	GTCTCCCTGG	AACAAAATGC	TGNAAAAGC	CATGAGGAGG	300
	CCAAGAAGCT	GCTGTGGCNG	ANGCGGATTC	AGAAAGGGCT	CCCTCATCAG	AGANGTGCAGA	360
	CATGTAAACC	AAATTAAACT	ATGGTGTCCA	ANGATAN			397